

论著

湖北钉螺线粒体基因组全序列测定研究

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摘要

目的 测定并分析湖北钉螺 (*Oncomelania hupensis*) 线粒体基因组全序列。方法 利用特异引物和通用引物分别扩增湖北钉螺线粒体细胞色素C氧化酶 I (CO I)、细胞色素b (Cytb)、16SrRNA (16S) 和细胞色素C氧化酶III (COIII) 基因片段,在此基础上利用长PCR技术扩增上述4个基因间的长片段,纯化克隆后采用引物步移法测序。结果 湖北钉螺线粒体基因组全序列为15 182 bp (GenBank登记号为FJ997214),为闭合环状分子,A+T含量为67.3%;包括13个蛋白基因、22个tRNA基因、2个rRNA基因和一段72 bp的A+T富集区;蛋白质编码基因均以ATG为启动子,除呼吸链NADH脱氢酶的第一亚单位 (ND1) 基因以潜在的T作为终止密码子外,其余基因均以典型的TAA或TAG为终止子;基因重叠区有2处,分别为4 bp和7 bp;基因间隔区共21处合计145 bp,长度范围为1~30 bp;22个tRNA中,除2个tRNASer和tRNAGln、tRNAIle以外均能形成典型的二级结构。结论 获得了湖北钉螺的线粒体基因组全序列。

关键词

湖北钉螺 线粒体基因组 引物步移法 序列分析

分类号

Complete Mitochondrial Genome Sequence of *Oncomelania hupensis* (Gastropoda: Rissooidea)

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Abstract

Objective To sequence and analyze the complete nucleotide sequence of the mitochondrial genome of *Oncomelania hupensis*. Methods Four long fragments were amplified by long PCR using the primers designed based on mtDNA-CO I, Cytb, 16S rRNA and COIII gene sequences, and sequenced by conserved primer-walking. Results The mitochondrial genome (GenBank accession no. FJ997214) was a circular molecule of 15 182 bp with a total A+T content of 67.32%, and contained 13 protein-coding genes, 2 ribosomal RNA genes, 22 tRNA genes, and an A+T-rich region of 72 bp. All 13 protein-coding genes of the *O. hupensis* mtDNA used ATG as start codon. Canonical TAA and TAG termination codons were found in 12 protein-coding genes, and the remaining one (ND1) had an incomplete termination codon (T). Two short gene overlaps were found with a length of 4 bp and 7 bp, respectively. The length of 21 total intergenic region of mtDNA was 145 bp ranging from 1-30 bp. A total of 22 transferring RNA were found, all of which were typical cloverleaf structure except for two tRNASer, one tRNAGln and one tRNAIle. Conclusion The complete sequence of *O. hupensis* mitochondrial genome has been determined.

Key words

[Oncomelania hupensis](#) [Mitochondrial genome](#) [Primer-walking](#) [Sequence analysis](#)

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